

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.0465 Seconds

(without alignments)  
837.928 Million cell updates/sec

Title: US-09-622-613b-13

Perfect score: 532

Sequence: 1 MSMDLTFQKKHLNTRDVC.....FCVTCENQAPVHFVGHC 105

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_73:\*

1: pirl:\*

2: pirl:\*

3: pirl:\*

4: pirl:\*

5: pirl:\*

6: pirl:\*

7: pirl:\*

8: pirl:\*

9: pirl:\*

10: pirl:\*

11: pirl:\*

12: pirl:\*

13: pirl:\*

14: pirl:\*

15: pirl:\*

16: pirl:\*

17: pirl:\*

18: pirl:\*

19: pirl:\*

20: pirl:\*

21: pirl:\*

22: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	551	94.7	104	2 A39035	ribonuclease-relat
2	287	49.3	111	2 A27121	ribonuclease-relat
3	280.5	48.2	111	1 JX0120	pancreatic ribonuc
4	264.5	45.4	111	2 JX0085	pancreatic ribonuc
5	144	24.7	119	2 S41111	pancreatic ribonuc
6	132	22.7	124	1 NRUI	angiotensin [valida
7	128	22.0	125	1 A32474	pancreatic ribonuc
8	126	21.6	128	1 NRCU	pancreatic ribonuc
9	125	21.5	124	1 NRKH	pancreatic ribonuc
10	120	20.6	128	1 NRKS	pancreatic ribonuc
11	120	20.5	128	1 NRGB	pancreatic ribonuc
12	119.5	20.5	145	1 A35332	angiotensin precurs
13	118	20.3	124	1 NRCA	pancreatic ribonuc
14	117	20.1	128	1 NRXY	pancreatic ribonuc
15	116	19.9	125	1 B43825	angiotensin - rabbi
16	114	19.6	124	1 NRHP	pancreatic ribonuc
17	113	19.4	147	1 NRHJAG	angiotensin precurs
18	112	19.2	124	1 NRBOB	pancreatic ribonuc
19	112	19.2	124	1 NRPG	pancreatic ribonuc
20	112	19.2	124	2 JCS560	pancreatic ribonuc
21	112	19.2	128	1 NRPO	pancreatic ribonuc
22	112	19.2	150	1 NRBO	pancreatic ribonuc
23	111.5	19.2	147	2 I52489	ribonuclease 4 (EC
24	111	19.1	124	2 S08549	ribonuclease - dom
25	111	19.1	128	1 NRHO	pancreatic ribonuc
26	111	19.1	167	2 S20065	pancreatic-type ri
27	110.5	19.0	123	1 A43825	angiotensin - pig
28	110.5	19.0	155	2 JCS6159	eosinophil associa
29	110	18.9	124	1 NRGA	pancreatic ribonuc

283224

## ALIGNMENTS

30	110	18.9	156	2 JC6160	eosinophil associa
31	109	18.7	124	1 NRSH	pancreatic ribonuc
32	109	18.7	124	1 NRPH	pancreatic ribonuc
33	109	18.7	124	2 S07141	pancreatic ribonuc
34	108	18.6	124	1 NRWB	pancreatic ribonuc
35	108	18.6	124	1 NRGN	pancreatic ribonuc
36	107	18.4	124	1 NRGF	pancreatic ribonuc
37	105	18.0	124	1 NRDEO	pancreatic ribonuc
38	105	18.0	124	1 NRDM	pancreatic ribonuc
39	105	18.0	124	1 NRCA	pancreatic ribonuc
40	105	18.0	124	1 NRCA	pancreatic ribonuc
41	105	18.0	124	1 NRCA	pancreatic ribonuc
42	104	17.9	124	1 NRHW	pancreatic ribonuc
43	103	17.7	124	1 NRDR	pancreatic ribonuc
44	103	17.7	124	1 NRDR	pancreatic ribonuc
45	103	17.7	124	1 NRKN	pancreatic ribonuc

## RESULT 1

A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C:Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 30-Jun-1993

C:Accession: A39035

R:Rardelt, W.; Mikulski, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match 94.7%; Score 551; DB 2; Length 104;  
Best Local Similarity 96.1%; Pred. No. 2.4e-48;  
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPKAICKGIASKNVLTTTS 62  
DB 2 DWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPKAICKGIASKNVLTTTS 61

QY 63 EFTLSDCNVTSRPEKYLKSTNFTCYTCENQAPVHFVGHC 105  
DB 62 EFTLSDCNVTSRPEKYLKSTNFTCYTCENQAPVHFVGHC 104

## RESULT 2

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kanauchi, H.; Takayan

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <RTT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 49.3%; Score 287; DB 2; Length 111;  
Best Local Similarity 49.1%; Pred. No. 8e-22;  
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFTYSRPEPKAICKGIASKNVL 58  
DB 2 DWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFTYSRPEPKAICKGIASKNVL 57

OY 59 LTTSEFYISDC---NVTSPCKYKLLKSTNFCVTCENQAVHFGVCHC 105  
Db 61 LSTRFOIINTCTRTSTPRCPYSSRPTETNIVICVKNQYVHFGAGIGRC 110

## RESULT 3

JX0120  
ribonuclease-related static acid-binding lectin - Japanese frog  
C:Species: Rana japonica (Japanese frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JX0120  
R:Kamaya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990  
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.  
A:Reference number: JX0120; MUID:91035319; PMID:2229005  
A:Accession: JX0120  
A:Molecule type: protein  
A:Residues: 1-111 <KAM>  
A:Experimental source: egg  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: lectin; pyroglytamic acid  
F:1/Modified site: pyroglutamate bonds: #status experimental  
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 48.2%; Score 280.5; DB 1; Length 111;  
Best Local Similarity 44.5%; Pred. No. 3.6e-21;  
Matches 49; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

OY 3 DMLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFYSPPEPKAICGIASKNV 58  
Db 2 NMAKFEKHIPNTSINCTIMDKSIYVGGCKERTFTISSATVKAICSGASTNRNV 61  
OY 59 LTTSEFYISDC---NVTSPCKYKLLKSTNFCVTCENQAVHFGVCHC 105  
Db 62 LSTRFOIINTCTRTSTPRCPYSSRPTETNIVICVKNQYVHFGAGIGRC 111

## RESULT 4

JX0085  
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Aug-1994  
C:Accession: JX0085  
R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, J. Biochem. 106, 729-735, 1989  
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.  
A:Reference number: JX0085; MUID:90130374; PMID:2613682  
A:Accession: JX0085  
A:Molecule type: protein  
A:Residues: 1-111 <NT>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: hydrolase; pyroglytamic acid  
F:1/Modified site: pyroglutamate bonds: #status experimental  
F:10-35,104/Active site: His, Lys, His #status predicted  
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 45.4%; Score 264.5; DB 2; Length 111;  
Best Local Similarity 42.7%; Pred. No. 1.4e-19;  
Matches 47; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

OY 3 DMLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFYSPPEPKAICGIASKNV 58  
Db 2 NMAKFEKHIPNTSINCTIMDKSIYVGGCKERTFTISSATVKAICSGASTNRNV 61  
OY 59 LTTSEFYISDC---NVTSPCKYKLLKSTNFCVTCENQAVHFGVCHC 105  
Db 62 LSTRFOIINTCTRTSTPRCPYSSRPTETNIVICVKNQYVHFGAGIGRC 111

RESULT 5  
S4111  
pancreatic ribonuclease - common iguana

C:Species: Iguana iguana (common iguana)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Aug-1998  
C:Accession: S4111  
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.  
Eur. J. Biochem. 219, 641-646, 1994  
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.  
A:Reference number: S4111; MUID:94139745; PMID:8307028  
A:Accession: S4111  
A:Molecule type: protein  
A:Residues: 1-119 <ZHA>  
C:Superfamily: pancreatic ribonuclease

Query Match 24.7%; Score 144; DB 2; Length 119;  
Best Local Similarity 30.1%; Pred. No. 1.9e-07;  
Matches 34; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

OY 3 DMLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFYSPPEPKAICGIASKNV 58  
Db 2 NMAKFEKHIPNTSINCTIMDKSIYVGGCKERTFTISSATVKAICSGASTNRNV 61  
OY 59 LTTSEFYISDC---NVTSPCKYKLLKSTNFCVTCENQAVHFGVCHC 105  
Db 62 LSTRFOIINTCTRTSTPRCPYSSRPTETNIVICVKNQYVHFGAGIGRC 111

## RESULT 6

JX0082  
pancreatic ribonuclease (EC 3.1.27.5) - cuis  
N:Alternate names: RNase A  
C:Species: Galea musteloides (cuis)  
C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 04-Oct-1996  
C:Accession: A00827  
R:Beintema, J.J.; Neuteboom, B.  
J. Mol. Evol. 19, 145-152, 1983  
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the  
A:Reference number: A92957; MUID:87036770; PMID:6571219  
A:Accession: A00827  
A:Molecule type: protein  
A:Residues: 1-124 <BEI>  
A:Note: About one-third of the molecules lacked Ala-1  
C:Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:16-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:94/Binding site: carboxylate (Asn) (covalent) #status absent

Query Match 22.7%; Score 132; DB 1; Length 124;  
Best Local Similarity 30.6%; Pred. No. 3.2e-06;  
Matches 38; Conservative 18; Mismatches 36; Indels 32; Gaps 7;

OY 2 DMLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFYSPPEPKAICGIASKNV 51  
Db 3 SSAMKFOGHNDSDHPTINTN--YCNEMARRSMTGRCRKFVNTFVEPLEAVQAVC-- 58  
OY 52 IIAKKNV-----LTTSEFYISDCNVTSPCKYKLLKSTNFCVTCENQAVHFGVCHC 105  
Db 59 --SOKNVPCCKNQGTWCYQSHSSMRITDCRVYSSSKYPCSYRMQQAQSIIVACGRTSV 116  
OY 96 PVHF 99  
Db 117 PVHF 120

RESULT 7  
A32474  
angiogenin (validated) - bovine  
N:Alternate names: angiogenesis factor  
N:Contains: ribonuclease (EC 3.1.27.-)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 25-Sep-1989 #sequence\_revision 25-Sep-1989 #text\_change 15-Sep-2000  
C:Accession: A32474; S02001; A30044; S48212

R:Bond, M.D.: Strydom, D.J.  
 Biochemistry 28, 6110-6113, 1989  
 A:Title: Amino acid sequence of bovine angiotensin.  
 A:Reference number: A32474; MUID:89375344; PMID:2775757  
 A:Accession: A32474  
 A:Molecule type: protein  
 A:Residues: 1-125 <BON>  
 A:Experimental source: plasma  
 R:Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.  
 FEBS Lett. 241, 41-45, 1988  
 A:Title: The complete amino acid sequence of bovine milk angiotensin.  
 A:Reference number: 502001; MUID:89065101; PMID:3197838  
 A:Accession: 502001  
 A:Molecule type: protein  
 A:Residues: 1-125 <MAE>  
 A:Experimental source: milk  
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallée, B.L.  
 Submitted to the Brookhaven Protein Data Bank, January 1995  
 A:Reference number: A65065; PDB:1NGI  
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125  
 Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995  
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallée, B.L.  
 A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.  
 A:Reference number: A58315; MUID:95224057; PMID:7708754  
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms  
 R:Lequin, O.; Alparé, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
 Submitted to the Brookhaven Protein Data Bank, April 1996  
 A:Reference number: A65709; PDB:13IO  
 A:Contents: annotation; conformation by (1)H-NMR, residues 1-125  
 R:Lequin, O.; Alparé, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
 Biochemistry 35, 8870-8880, 1996  
 A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spect  
 A:Reference number: A58821; MUID:96280645; PMID:8688423  
 A:Contents: annotation; conformation by (1)H-NMR  
 R:Reisdorf, C.; Aberger, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.  
 Eur. J. Biochem. 224, 811-822, 1994  
 A:Title: Proton resonance assignments and secondary structure of bovine angiotensin.  
 A:Reference number: S48212; MUID:95010071; PMID:7925406  
 A:Contents: annotation; conformation by (1)H-NMR  
 C:Function:  
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: angiotensin; hydrolase; nucleic acid degradation  
 F:60-66/Region: receptor binding #status predicted  
 F:14,41,119/Active site: His, Lys, His #status predicted  
 F:27-82,40-93,58-108/disulfide bonds: #status experimental  
 Query Match 22.0%; Score 128; DB 1; Length 125;  
 Best Local Similarity 34.0%; Pred. No. 8.2e-06;  
 Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;  
 Oy 17 DVDCNNIMSTNLF--HCKDKNTFIYSRPEPKAICGIIASKN-----VLTSFYL 66  
 Db 24 DECFPMNKNRRLTPRCKDKNTFIHGKNNDKAIK---DRNGQPYRGDLRISKSEFOI 79  
 Oy 67 SDC---NVTSR-PCKYKLRKSTNFCVTCENQAPVHF 99  
 Db 80 TCKHKGSSRPRCRGATFDSKVIYVGCENGLPVHF 116  
 RESULT 8  
 NRCU  
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Myocystocoypus (nutria, coypu)  
 C:Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
 C:Accession: A00822  
 R:Van den Berg, A.; Van den Hende-Timmer, L.; Beintema, J.J.  
 Biochim. Biophys. Acta 453, 400-409, 1976  
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
 A:Reference number: A90612; MUID:77065676; PMID:999896  
 A:Accession: A00822  
 A:Molecule type: protein

A:Residues: 1-128 <VAN>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:12,41,119/Active site: His, Lys, His #status predicted  
 F:26-84,40-95,58-110,65-72/disulfide bonds: #status predicted  
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 Query Match 21.6%; Score 126; DB 1; Length 128;  
 Best Local Similarity 29.9%; Pred. No. 1.3e-05;  
 Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;  
 Oy 7 FOKKHL-----TNRDVCNNIM-STNLF--HCKDKNTFIYSRPEPKAICGIIASKN 58  
 Db 8 FERQHMDSCSPSTNPVYCNEMKSRMTGRCRKPVTVEHPLADQAVC-----EQKNV 63  
 Oy 59 L-----TTSEFLSDCNVTSRP---CKYKLRKSTNFCVTCENQ--APVHF 99  
 Db 64 LCRNGQTCYOSNSNMHITDCRVTNSDYPNCSFRISOEKSIVVACEGNRPVPHF 120  
 RESULT 9  
 NRCUK  
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale  
 N:Alternate names: RNase A  
 C:Species: Balaeoptera acutorostrata (minke whale, lesser rorqual)  
 C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
 C:Accession: A00818  
 R:Emmens, M.; Wellling, G.W.; Beintema, J.J.  
 Biochem. J. 157, 317-323, 1976  
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea  
 A:Reference number: A00818; MUID:76277855; PMID:962870  
 A:Accession: A00818  
 A:Molecule type: protein  
 A:Residues: 1-124 <EMM>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:12,41,119/Active site: His, Lys, His #status predicted  
 F:26-84,40-95,58-110,65-72/disulfide bonds: #status predicted  
 F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental  
 Query Match 21.5%; Score 125; DB 1; Length 124;  
 Best Local Similarity 28.6%; Pred. No. 1.6e-05;  
 Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;  
 Oy 5 LTFOKKHLTNRDVC-----CNNIMSTNLF--HCKDKNTFIYSRPEPKAICGIIASK 56  
 Db 6 MKFQROHMDSCSPGNPNVYCNEMKSRMTGRCRKPVTVEHSELDVAVAC---SQK 61  
 Oy 57 NVL-----TTSEFLSDCNVTSRP---CKYKLRKSTNFCVTCENQ--APVHF 99  
 Db 62 NVLCKNRTNCTYESNSMTHTDRCROTSSKRYPCAVYTSQKXKHIIYACGNGRPVPHF 120  
 RESULT 10  
 NRS  
 pancreatic ribonuclease (EC 3.1.27.5) - casiragua  
 C:Species: Proechimys quaitrae (casiragua)  
 C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 30-Sep-1993  
 C:Accession: A00821  
 R:Beintema, J.J.; Knol, G.; Martena, B.  
 Biochim. Biophys. Acta 705, 102-110, 1982  
 A:Title: The primary structures of pancreatic ribonucleases from African porcupine an  
 A:Reference number: A90644; MUID:83000399; PMID:7115727  
 A:Accession: A00821  
 A:Molecule type: protein  
 A:Residues: 1-128 <BEI>  
 A:Note: residues 67-78 were positioned primarily by homology with other ribonucleases  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:12,41,119/Active site: His, Lys, His #status predicted  
 F:26-84,40-95,58-110,65-72/disulfide bonds: #status predicted  
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Query Match          20.6% Score 120; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No.5.3e-05;
Matches      35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

OY 7 FOKKHL-----TNTRDVDCNNIM--STNLF--HCKDKNFIFYSRPEPYKAIGKIASKNV 58
    ||:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 FORGHIDSSGSTPNPNCNAMKSRNMTQERCKPVNFVEHPLADVOAVC----FOKNV 63

OY 59 -----LTTSEFYLSDCNVTSR---PCKYLKKSTNFTVCYCENQ--APVHF 99
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 PCKNGSNCSCESTSMMHTDCLRTLSNSKFPDCLVRTSQEKSIIIVACGNGPYVPVHF 120

RESULT 11
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N:Alternate names: RNase IB
C:Species: Cavia porcellus (guinea pig)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A00826
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.
Eur. J. Biochem. 75, 91-100, 1977
A>Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure
A:Reference number: A91247; MUID:77185023; PMID:862624
A:Accession: A00826
A:Molecule type: Protein
A:Residues: 1-128 <VAN>
A>Note: 64-Pro was also found
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:21.34/Binding site: carbonylate (Asn), His #status predicted
F:26-84,40-95,58-110,65-72/disulfide bonds: #status predicted

Query Match          20.6% Score 120; DB 1; Length 128;
Best Local Similarity 28.5%; Pred. No.5.3e-05;
Matches      35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;

OY 2 SDWLTFQKKHL-----TNTRDVDCNNIM--STNLFPHCKDKNFITYSRPEPYKAIGKI 52
    ||:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 SSAMKFORQHMDPEGSPSSNSNY-CNVMMIRRNMTQGRCRPVNTFVHESLADVOAVC-- 58

OY 53 IASKNVL-----LTTSEFYLSDCNVTSRP---CKYLLKSTNFTVCYCENQ--AP 96
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 -FOKNVLCKCGQTNCYOSYSRRITDCRVTSRSSKFPNCSTRMSOAOKSIIVACEGDPPYP 117

OY 97 VHF 99
    |||
Db 118 VHF 120

RESULT 12
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A>Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2227458
A:Accession: A35932
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
C:Function:
A>Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease

```

C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglyutamic acid  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-145/Product: angiogenin #status predicted <MAT>  
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:37,64,137/Active site: His, Lys, His #status predicted  
F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 20.5%; Score 119.5; DB 1; Length 145;  
Best Local Similarity 30.8%; Pred. No. 6,8e-05;  
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;

Qy 10 KHLTTRD-----CNIIMSTNLF-HCKDKNTFYISREPVKAIC--KILISK 57  
Db 32 KFLTTHHAKPKGRDRYCEIRMKRRSLTSPCKDVFNTFHNKSNIKAIKANGSPYREN 91  
Qy 58 V-LTTFSEFLSDCNTVS---RPCKRKLRKSTNTFCVCEADAVHF 99  
Db 92 LMSKSPFOVYTTCKHTGGSPREPCOYRASAGFRHVIYVACENGLEPVHF 138

RESULT 13  
NRCB  
pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicauda (tentative sequence)  
N:Alternate names: RNase 1; RNase A  
C:Species: Chinchilla brevicauda, Chinchilla lanigera brevicauda  
C:Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
A:Accession: A00820  
R:Van den Berg, A.; van den Hende-Timmer, L.; Belintema, J.J.  
Biochim. Biophys. Acta 453, 400-409, 1976  
A:Title: Isolation, properties and primary structure of coryu and chinchilla pancrea  
A:Reference number: A90612; MUID:77065676; PMID:999896  
A:Accession: A00820  
A:Molecule type: protein  
A:Residues: 1-124 <VAN>  
A:Note: a second component of chinchilla ribonuclease has 32-Asp  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,110-65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carbonylate (Asn) (covalent) #status experimental

Query Match 20.3%; Score 118; DB 1; Length 124;  
Best Local Similarity 27.0%; Pred. No. 8.2e-05;  
Matches 33; Conservative 19; Mismatches 42; Indels 28; Gaps 6;

Qy 2 SDMLTFQKHL-----TNRDVCNNIM---STNLFHCKDKNTFYISREPVKAICKGI 53  
Db 3 SSAMFQKHMDSSGSPSTNANYCNEMKGRNMGTGCKPVNTFVHEPLADYQAVC--- 58  
Qy 54 ASKNV-----LTTSEFLSDCNTVSRP---CKYILKSTNTFCVTCENQ--APV 97  
Db 59 FQKNVPCNCGSNCGSNCSNMHITDCRITLSKYPNCYSYKRSRENKGLIYACENPVYPV 118  
Qy 98 HF 99  
Db 119 HF 120

RESULT 14  
NRY  
pancreatic ribonuclease (EC 3.1.27.5) - capybara  
N:Alternate names: RNase 1; RNase A  
C:Species: Hydrochaeris hydrochaeris (capybara, capylincho)  
C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 29-Oct-1999  
A:Accession: A00824  
R:Belintema, J.J.; Neuteboom, B.  
J. Mol. Evol. 19, 145-152, 1983  
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the  
A:Reference number: A92957; MUID:87036770; PMID:6571219  
A:Accession: A00824  
A:Molecule type: protein  
A:Residues: 1-128 <BEI>  
C:Superfamily: pancreatic ribonuclease

C:Keywords: hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/disulfide bonds: #status predicted

## Query Match

20.18; Score 117; DB 1; Length 128;  
Best Local Similarity 28.08; Pred. No. 0.00011;

Matches 33; Conservative 21; Mismatches 44; Indels 20; Gaps 6;

OY 2 SDMLFFQKKHL-----TNRDVCNNIMSTNLF---HCKDKNTFYSRPEPKAIC-KGI 52  
| : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 3 SSAMKFGROHVDSSGSSSNANVCNEMVRRKKTODCKRPVNTFVHEPLADVOAVCFQKN 62

OY 53 IASKNVLTF-----SEFYISDCNVTSR---PCKYKLRKSTNFCVTCENQ--APVHF 99  
| : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 63 VPCKHGTNTCYQSYSSMHTDCRYTNSKFPDCSYRTTOAKSIVVACEGNLVYPVHF 120

## RESULT 15

B43825

angiotensin - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999

C:Accession: S29833; B43825

R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.  
Biochim. Biophys. Acta 1162, 177-186, 1993.

A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discenime  
A:Reference number: S29833; MUID:93192291; PMID:8448182

A:Accession: S29833

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-125 <BON>

A:Note: submitted to the Protein Sequence Database, December 1992

C:Superfamily: pancreatic ribonuclease

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

## Query Match

19.98; Score 116; DB 1; Length 125;  
Best Local Similarity 31.28; Pred. No. 0.00013;

Matches 24; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

OY 31 CKDKNTFYSRPEPKAICK---GIASKNV-LTSEFYISDCNVT---RPCKYKLRK 82  
| ||| ||| : : : : : ||| : : : : : ||| : : : : :  
Db 39 CKDKNTFYHGNKSGIKVDCKDKNGKPYGKNFRISKSFOYTTCKHVGSGPWPCCRYRATS 98

OY 83 STNFCVTCENQAPVHF 99  
| : ||| : ||| |||  
Db 99 GSRNIVACENGLPVHF 115

Search completed: June 25, 2003, 14:58:04  
Job time : 13.0465 secs

